

In the claims:

- 1. (Presently Canceled)
- 2-7. (Previously Canceled)
- 8. (Presently Canceled)
- 9-18. (Previously Canceled)
- 19-22. (Presently Canceled)
- 23. (Previously Canceled)
- 24-51. (Presently Canceled)

52. (New): A method for identifying a compound which binds to a polypeptide selected from the group consisting of:

a) a polypeptide which is at least 90% identical to the amino acid sequence of SEQ ID NO:47;

b) a polypeptide which is at least 90% identical to the amino acid sequence of SEQ ID NO:49;

c) a polypeptide which is at least 90% identical to residues 15-423 of the amino acid sequence of SEQ ID NO:47;

d) a polypeptide which is at least 90% identical to the amino acid sequence encoded by the cDNA insert of clone EpT294, which was deposited with ATCC as Accession Number 207220; and

e) a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 90% identical to the nucleotide sequence of SEQ ID NO:45 or SEQ ID NO:46; wherein the polypeptide exhibits lipase activity;

the method comprising:

- i) contacting the polypeptide with a test compound under conditions suitable for binding; and
 - ii) detecting binding of the test compound to the polypeptide;
- thereby identifying a compound which binds to the polypeptide.

53. (New): The method of claim 52, wherein the polypeptide further comprises heterologous sequences.

54. (New): The method of claim 52, wherein the polypeptide is an isolated polypeptide, a membrane-bound form of an isolated polypeptide or a cell comprising the polypeptide.

55. (New): The method of claim 54, wherein the cell is a mammalian cell.

56. (New): The method of claim 52, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

- a) direct detection of test compound/polypeptide binding;
- b) a competition binding assay;
- c) an immunoassay; and
- d) a yeast two-hybrid assay.

57. (New): The method of claim 52, wherein the binding of the test compound to the polypeptide is detected is by an assay for an activity of the polypeptide.

58. (New): The method of claim 57, wherein the assay for activity is selected from the group consisting of:

- a) an assay for measuring formation of ester bonds between a fatty acid and a lipid moiety;
- b) an assay for measuring breakage of ester bonds between a fatty acid and a lipid moiety;
- c) an assay for measuring fat absorption;
- d) an assay for measuring fat metabolism; and
- e) an assay for measuring eicosanoid synthesis.

59. (New): A method for identifying a compound which binds to a polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:47;
- b) a polypeptide comprising the amino acid sequence of SEQ ID NO:49;

c) a polypeptide comprising residues 15-423 of the amino acid sequence of SEQ ID NO:47;

d) a polypeptide comprising the amino acid sequence encoded by the cDNA insert of clone EpT294, which was deposited with ATCC as Accession Number 207220; and

e) a polypeptide comprising the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO:45 or SEQ ID NO:46;

the method comprising:

i) contacting the polypeptide with a test compound under conditions suitable for binding; and

ii) detecting binding of the test compound to the polypeptide;
thereby identifying a compound which binds to the polypeptide.

60. (New): The method of claim 59, wherein the polypeptide further comprises heterologous sequences.

61. (New): The method of claim 59, wherein the polypeptide is an isolated polypeptide, a membrane-bound form of an isolated polypeptide or a cell comprising the polypeptide.

62. (New): The method of claim 61, wherein the cell is a mammalian cell.

63. (New): The method of claim 59, wherein the binding of the test compound to the polypeptide is detected by a method selected from the group consisting of:

- a) direct detection of test compound/polypeptide binding;
- b) a competition binding assay;
- c) an immunoassay; and
- d) a yeast two-hybrid assay.

64. (New): The method of claim 59, wherein the binding of the test compound to the polypeptide is detected by an assay for an activity of the polypeptide.

65. (New): The method of claim 64, wherein the assay for activity is selected from the group consisting of:

- a) an assay for measuring formation of ester bonds between a fatty acid and a lipid moiety;
- b) an assay for measuring breakage of ester bonds between a fatty acid and a lipid moiety;
- c) an assay for measuring fat absorption;
- d) an assay for measuring fat metabolism; and
- e) an assay for measuring eicosanoid synthesis.

66. (New): A method for identifying a compound which modulates the activity of a polypeptide selected from the group consisting of:

a) a polypeptide which is at least 90% identical to the amino acid sequence of SEQ ID NO:47;

b) a polypeptide which is at least 90% identical to the amino acid sequence of SEQ ID NO:49;

c) a polypeptide which is at least 90% identical to residues 15-423 of the amino acid sequence of SEQ ID NO:47;

d) a polypeptide which is at least 90% identical to the amino acid sequence encoded by the cDNA insert of clone EpT294, which was deposited with ATCC as Accession Number 207220; and

e) a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 90% identical to the nucleotide sequence of SEQ ID NO:45 or SEQ ID NO:46; wherein the polypeptide exhibits lipase activity;

the method comprising:

- i) contacting the polypeptide with a test compound; and
- ii) comparing the effect on the activity of the polypeptide in the presence of the test compound to the effect on the activity of the polypeptide in the absence of the test compound;

thereby identifying a compound which modulates the activity of the polypeptide.

67. (New): The method of claim 66, wherein the polypeptide further comprises heterologous sequences.

68. (New): The method of claim 66, wherein the polypeptide is an isolated polypeptide, a membrane-bound form of an isolated polypeptide or a cell comprising the polypeptide.

69. (New): The method of claim 68, wherein the cell is a mammalian cell.

70. (New): The method of claim 66, wherein the activity of the polypeptide is selected from the group consisting of:

- a) esterification of fatty acids or lipid moieties;
- b) de-esterification of fatty acids or lipid moieties;
- c) fat absorption;
- d) fat metabolism; and
- e) eicosanoid synthesis.

71. (New): A method for identifying a compound which modulates the activity of a polypeptide selected from the group consisting of:

- a) a polypeptide comprising the amino acid sequence of SEQ ID NO:47;
- b) a polypeptide comprising the amino acid sequence of SEQ ID NO:49;
- c) a polypeptide comprising residues 15-423 of the amino acid sequence of SEQ ID NO:47;
- d) a polypeptide comprising the amino acid sequence encoded by the cDNA insert of clone EpT294, which was deposited with ATCC as Accession Number 207220; and
- e) a polypeptide comprising the amino acid sequence encoded by the nucleotide sequence set forth in SEQ ID NO:45 or SEQ ID NO:46;

the method comprising:

- i) contacting the polypeptide with a test compound; and
- ii) comparing the effect on the activity of the polypeptide in the presence of the test compound to the effect on the activity of the polypeptide in the absence of the test compound;

thereby identifying a compound which modulates the activity of the polypeptide.

72. (New): The method of claim 71, wherein the polypeptide further comprises heterologous sequences.

73. (New): The method of claim 71, wherein the polypeptide is an isolated polypeptide, a membrane-bound form of an isolated polypeptide or a cell comprising the polypeptide.

74. (New): The method of claim 73, wherein the cell is a mammalian cell.

75. (New): The method of claim 71, wherein the activity of the polypeptide is selected from the group consisting of:

- a) esterification of fatty acids or lipid moieties;
- b) de-esterification of fatty acids or lipid moieties;
- c) fat absorption;
- d) fat metabolism; and
- e) eicosanoid synthesis.